

IN SILICO

- Identification of testis-specific antigens in the publicly accessible total pool of full-length genes

WET BENCH

- Validation of testis-specificity
- Analysis of testis-specific genes in tumors

Fig. 1

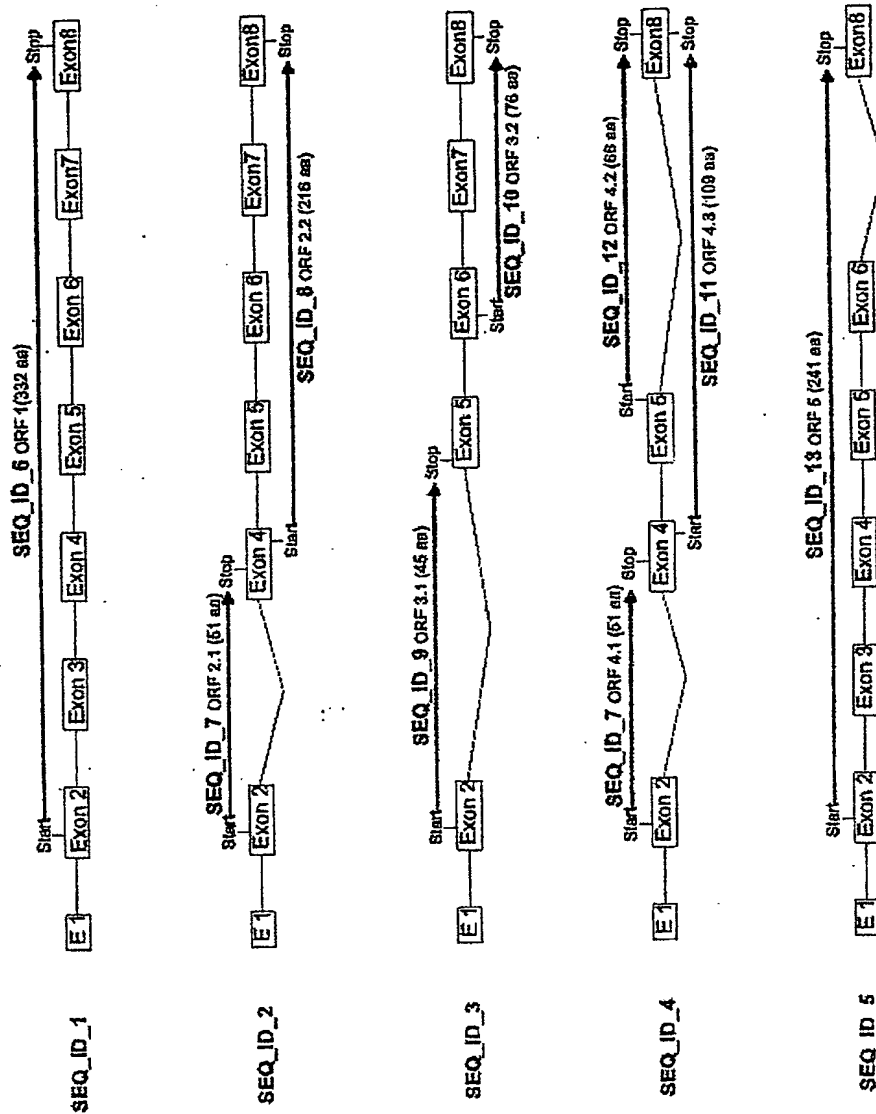


Figure 2

SEQ_ID_6 MSTVREQLIEKLIEDDENSQCKITIVGTGAVGACATSIILRLDLADELALVDVAIDKLGEMDLQHSLEFSTSKTTSCKDYSGAHSKIVIVDAGAQ 100
 SEQ_ID_13 MSTVREQLIEKLIEDDENSQCKITIVGTGAVGACATSIILRLDLADELALVDVAIDKLGEMDLQHSLEFSTSKTTSCKDYSGAHSKIVIVDAGAQ 100
 SEQ_ID_7 MSTVREQLIEKLIEDDENSQCKITIVGTGAVGACATSIILRLDLADELALVDVAIDKLGEMDLQHSLEFSTSKTTSCKDYSGAHSKIVIVDAGAQ 100
 SEQ_ID_9 MSTVREQLIEKLIEDDENSQCKITIVGTGAVGACATSIILRLDLADELALVDVAIDKLGEMDLQHSLEFSTSKTTSCKDYSGAHSKIVIVDAGAQ 100
 SEQ_ID_8 MSTVREQLIEKLIEDDENSQCKITIVGTGAVGACATSIILRLDLADELALVDVAIDKLGEMDLQHSLEFSTSKTTSCKDYSGAHSKIVIVDAGAQ 100
 SEQ_ID_11 -----
 SEQ_ID_10 -----
 SEQ_ID_12 -----

SEQ_ID_6 QGETKIALVQHVVAIAKSIIPATVHYSPDCKILVGNPNVDILTYIWKISGLPVTIVGSCNLDGSAHFYLLIGEKLGVKFTSCHGNI GEGHDSVPL 200
 SEQ_ID_13 QGETKIALVQHVVAIAKSIIPATVHYSPDCKILVGNPNVDILTYIWKISGLPVTIVGSCNLDGSAHFYLLIGEKLGVKFTSCHGNI GEGHDSVPL 200
 SEQ_ID_7 -----
 SEQ_ID_9 -----
 SEQ_ID_8 -----
 SEQ_ID_11 -----
 SEQ_ID_10 -----
 SEQ_ID_12 -----

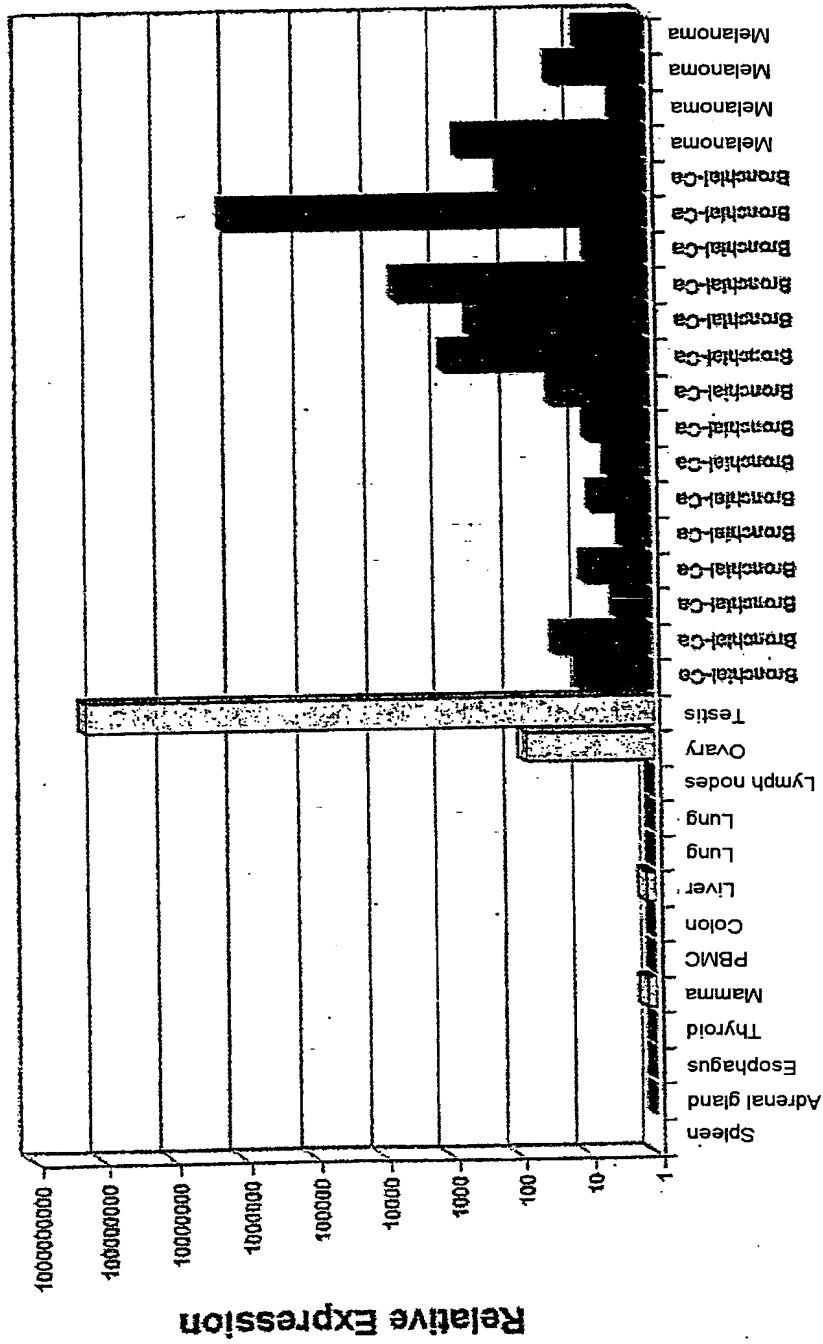
SEQ_ID_6 WSGVNVAGVALATLOPKLGTSDSKHWNHKKQVIQSAEYI IKLKVTSWALGLSVMDLVGSHLMLRRVHPVSTWVKGLNGTKEELFLSI PCVLGRGV 300
 SEQ_ID_13 WSGVNVAGVALATLOPKLGTSDSKHWNHKKQVIQSAEYI IKLKVTSWALGLSVMDLVGSHLMLRRVHPVSTWVKGLNGTKEELFLSI PCVLGRGV 300
 SEQ_ID_7 -----
 SEQ_ID_9 -----
 SEQ_ID_8 -----
 SEQ_ID_11 -----
 SEQ_ID_10 -----
 SEQ_ID_12 -----

SEQ_ID_6 SOWVKINLSSEALFKKSAETLWNIQDLIF 332
 SEQ_ID_13 SOWVKINLSSEALFKKSAETLWNIQDLIF 332
 SEQ_ID_7 -----
 SEQ_ID_9 -----
 SEQ_ID_8 SOWVKINLSSEALFKKSAETLWNIQDLIF 216
 SEQ_ID_11 SOWVKINLSSEALFKKSAETLWNIQDLIF 76
 SEQ_ID_10 SOWVKINLSSEALFKKSAETLWNIQDLIF 76
 SEQ_ID_12 SOWVKINLSSEALFKKSAETLWNIQDLIF 66

Laciale dehydrogenase, active site (framed)
 Tumor-specific epitopes (bold type)

Figure 3

LDHC quantitative Real-time PCR



Tissue

Figure 4

TPTE splice variants

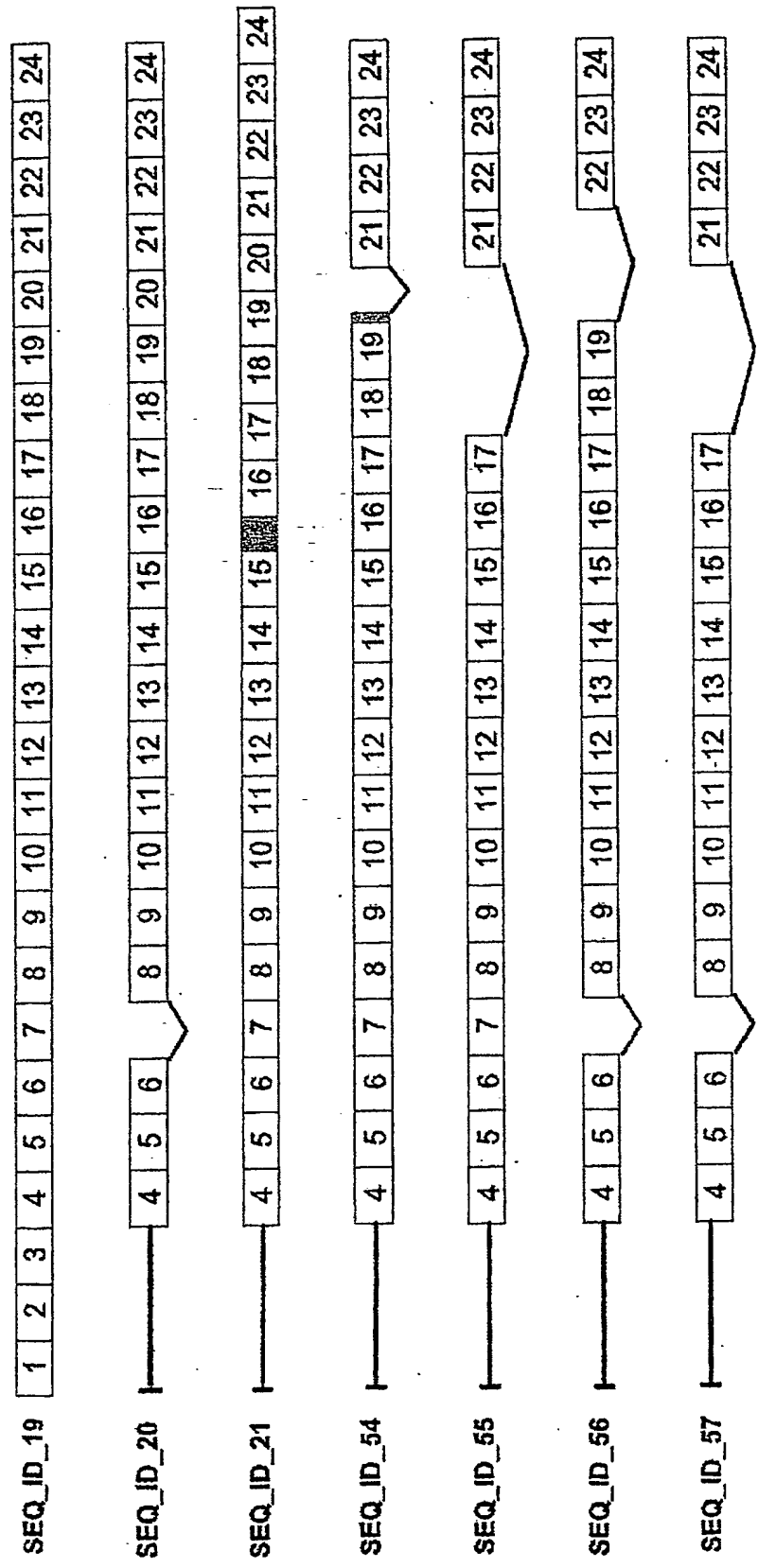


Figure 5

```

SEQ_ID_19 MNEFPDPTDLAGVIIELGPNDSPTSEFKGATEAPAKESPTSEFKGAARVSPISESVL 60
SEQ_ID_20 MNEFPDPTDLAGVIIELGPNDSPTSEFKGATEAPAKES-----VL 42
SEQ_ID_21 MNEFPDPTDLAGVIIELGPNDSPTSEFKGATEAPAKESPTSEFKGAARVSPISESVL 60
SEQ_ID_58 MNEFPDPTDLAGVIIELGPNDSPTSEFKGATEAPAKESPTSEFKGAARVSPISESVL 60
SEQ_ID_59 MNEFPDPTDLAGVIIELGPNDSPTSEFKGATEAPAKESPTSEFKGAARVSPISESVL 60
SEQ_ID_60 MNEFPDPTDLAGVIIELGPNDSPTSEFKGATEAPAKES-----VL 42
SEQ_ID_61 MNEFPDPTDLAGVIIELGPNDSPTSEFKGATEAPAKES-----VL 42

SEQ_ID_19 ARLSKFEVEDAENVASYDSKIKKIVBSIVSSFAFGVFLVLLDVTLILADLIPTOSKL 120
SEQ_ID_20 ARLSKFEVEDAENVASYDSKIKKIVBSIVSSFAFGVFLVLLDVTLILADLIPTOSKL 102
SEQ_ID_21 ARLSKFEVEDAENVASYDSKIKKIVBSIVSSFAFGVFLVLLDVTLILADLIPTOSKL 120
SEQ_ID_58 ARLSKFEVEDAENVASYDSKIKKIVBSIVSSFAFGVFLVLLDVTLILADLIPTOSKL 120
SEQ_ID_59 ARLSKFEVEDAENVASYDSKIKKIVBSIVSSFAFGVFLVLLDVTLILADLIPTOSKL 120
SEQ_ID_60 ARLSKFEVEDAENVASYDSKIKKIVBSIVSSFAFGVFLVLLDVTLILADLIPTOSKL 102
SEQ_ID_61 ARLSKFEVEDAENVASYDSKIKKIVBSIVSSFAFGVFLVLLDVTLILADLIPTOSKL 102

SEQ_ID_19 YIPLYRSISIALALFFIMOVLLRVFVERROQYFSDLFNILDTAIVILLVGVVYIFED 180
SEQ_ID_20 YIPLYRSISIALALFFIMOVLLRVFVERROQYFSDLFNILDTAIVILLVGVVYIFED 162
SEQ_ID_21 YIPLYRSISIALALFFIMOVLLRVFVERROQYFSDLFNILDTAIVILLVGVVYIFED 180
SEQ_ID_58 YIPLYRSISIALALFFIMOVLLRVFVERROQYFSDLFNILDTAIVILLVGVVYIFED 180
SEQ_ID_59 YIPLYRSISIALALFFIMOVLLRVFVERROQYFSDLFNILDTAIVILLVGVVYIFED 180
SEQ_ID_60 YIPLYRSISIALALFFIMOVLLRVFVERROQYFSDLFNILDTAIVILLVGVVYIFED 162
SEQ_ID_61 YIPLYRSISIALALFFIMOVLLRVFVERROQYFSDLFNILDTAIVILLVGVVYIFED 162

SEQ_ID_19 IKLLRNIPRWTHLLRLRLITLLRIIFELFHQKQLEKLIARRVSENKRRYTRDGFOLDIT 240
SEQ_ID_20 IKLLRNIPRWTHLLRLRLITLLRIIFELFHQKQLEKLIARRVSENKRRYTRDGFOLDIT 222
SEQ_ID_21 IKLLRNIPRWTHLLRLRLITLLRIIFELFHQKQLEKLIARRVSENKRRYTRDGFOLDIT 240
SEQ_ID_58 IKLLRNIPRWTHLLRLRLITLLRIIFELFHQKQLEKLIARRVSENKRRYTRDGFOLDIT 240
SEQ_ID_59 IKLLRNIPRWTHLLRLRLITLLRIIFELFHQKQLEKLIARRVSENKRRYTRDGFOLDIT 240
SEQ_ID_60 IKLLRNIPRWTHLLRLRLITLLRIIFELFHQKQLEKLIARRVSENKRRYTRDGFOLDIT 222
SEQ_ID_61 IKLLRNIPRWTHLLRLRLITLLRIIFELFHQKQLEKLIARRVSENKRRYTRDGFOLDIT 222

SEQ_ID_19 YUTERIAMSFPSSGRQSFYRNFKEVVRFLDKKRNHYRVYNLCS----- 286
SEQ_ID_20 YUTERIAMSFPSSGRQSFYRNFKEVVRFLDKKRNHYRVYNLCS----- 268
SEQ_ID_21 YUTERIAMSFPSSGRQSFYRNFKEVVRFLDKKRNHYRVYNLCSMYITLYCATVDREQ 300
SEQ_ID_58 YUTERIAMSFPSSGRQSFYRNFKEVVRFLDKKRNHYRVYNLCS----- 286
SEQ_ID_59 YUTERIAMSFPSSGRQSFYRNFKEVVRFLDKKRNHYRVYNLCS----- 286
SEQ_ID_60 YUTERIAMSFPSSGRQSFYRNFKEVVRFLDKKRNHYRVYNLCS----- 268
SEQ_ID_61 YUTERIAMSFPSSGRQSFYRNFKEVVRFLDKKRNHYRVYNLCS----- 268

SEQ_ID_19 ----ERAYDPKHFHNRVVRIMIDDBNVPTLHQMVVPTKEVNEHMAQOLENIVAIHCKGGT 342
SEQ_ID_20 ----ERAYDPKHFHNRVVRIMIDDBNVPTLHQMVVPTKEVNEHMAQOLENIVAIHCKGGT 324
SEQ_ID_21 ITARENAVDPKHFHNRVVRIMIDDBNVPTLHQMVVPTKEVNEHMAQOLENIVAIHCKGGT 360
SEQ_ID_58 ----ERAYDPKHFHNRVVRIMIDDBNVPTLHQMVVPTKEVNEHMAQOLENIVAIHCKGGT 342
SEQ_ID_59 ----ERAYDPKHFHNRVVRIMIDDBNVPTLHQMVVPTKEVNEHMAQOLENIVAIHCKGGT 342
SEQ_ID_60 ----ERAYDPKHFHNRVVRIMIDDBNVPTLHQMVVPTKEVNEHMAQOLENIVAIHCKGGT 324
SEQ_ID_61 ----ERAYDPKHFHNRVVRIMIDDBNVPTLHQMVVPTKEVNEHMAQOLENIVAIHCKGGT 324

SEQ_ID_19 DRGTGM/CAPLIASEICSTAKESLYYFGERRTDKTHSEKFGQVETPSQKRYVAYFAQVKH 402
SEQ_ID_20 DRGTGM/CAPLIASEICSTAKESLYYFGERRTDKTHSEKFGQVETPSQKRYVAYFAQVKH 384
SEQ_ID_21 DRGTGM/CAPLIASEICSTAKESLYYFGERRTDKTHSEKFGQVETPSQKRYVAYFAQVKH 420
SEQ_ID_58 DRGTGM/CAPLIASEICSTAKESLYYFGERRTDKTHSEKFGQVETPSQKRYVAYFAQVKH 395
SEQ_ID_59 G----- 343
SEQ_ID_60 DRGTGM/CAPLIASEICSTAKESLYYFGERRTDKTHSEKFGQVETPSQKRYVAYFAQVKH 370
SEQ_ID_61 G----- 325

SEQ_ID_19 LYNWNLPPRRILFIKRFIYISIPRYVRLDKIQIEMKKVVFSTISLGKCSVLNITTDKI 462
SEQ_ID_20 LYNWNLPPRRILFIKRFIYISIPRYVRLDKIQIEMKKVVFSTISLGKCSVLNITTDKI 444
SEQ_ID_21 LYNWNLPPRRILFIKRFIYISIPRYVRLDKIQIEMKKVVFSTISLGKCSVLNITTDKI 480
SEQ_ID_58 -----YVRDLKIQIEMKKVVFSTISLGKCSVLNITTDKI 379
SEQ_ID_59 -----SYLDNITTDKI 381
SEQ_ID_60 -----YVRDLKIQIEMKKVVFSTISLGKCSVLNITTDKI 361
SEQ_ID_61 -----YVRDLKIQIEMKKVVFSTISLGKCSVLNITTDKI 361

SEQ_ID_19 LIDVFDGPPLYDDVAVQFFYSNLPTYYDNCSTYFWLHTSFTEHNRILYLPANELDNLHOK 522
SEQ_ID_20 LIDVFDGPPLYDDVAVQFFYSNLPTYYDNCSTYFWLHTSFTEHNRILYLPANELDNLHOK 504
SEQ_ID_21 LIDVFDGPPLYDDVAVQFFYSNLPTYYDNCSTYFWLHTSFTEHNRILYLPANELDNLHOK 540
SEQ_ID_58 LIDVFDGPPLYDDVAVQFFYSNLPTYYDNCSTYFWLHTSFTEHNRILYLPANELDNLHOK 439
SEQ_ID_59 LIDVFDGPPLYDDVAVQFFYSNLPTYYDNCSTYFWLHTSFTEHNRILYLPANELDNLHOK 441
SEQ_ID_60 LIDVFDGPPLYDDVAVQFFYSNLPTYYDNCSTYFWLHTSFTEHNRILYLPANELDNLHOK 421
SEQ_ID_61 LIDVFDGPPLYDDVAVQFFYSNLPTYYDNCSTYFWLHTSFTEHNRILYLPANELDNLHOK 421

SEQ_ID_19 ARRIYPSDFAVEILFGEKNTSSDVVAGSD 531
SEQ_ID_20 ARRIYPSDFAVEILFGEKNTSSDVVAGSD 533
SEQ_ID_21 ARRIYPSDFAVEILFGEKNTSSDVVAGSD 569
SEQ_ID_58 -----
SEQ_ID_59 ARRIYPSDFAVEILFGEKNTSSDVVAGSD 468
SEQ_ID_60 ARRIYPSDFAVEILFGEKNTSSDVVAGSD 470
SEQ_ID_61 ARRIYPSDFAVEILFGEKNTSSDVVAGSD 450

```

Figure 6

[illegible]

Fig. 7a

1	SEQ_31	TGGAAAAATCACACTGACCTGTGTGTATATTAACAGGTTACATGSAITGAGAACTGTGCAAAAATAATCTTTTTCACAAAATCCAGATTCT	695
2	SEQ_32	TGGAAAAAACCACACTACTCTGTGTGTATATTAACAGGTTACATGSAITGAGAACTGTGCAAAAATAATCTTTTTCACAAAATCCAGATTCT	719
3	SEQ_33	TGGAAAAATTCAGACTGACTCTGTGTGTATATTAACAGGTTACATGSAITGAGAACTGTGCAAAAATAATCTTTTTCACAAAATCCAGATTCT	674
4	SEQ_29	TGGAAAAATCACACTGACCTGTGTGTATATTAACAGGTTACATGSAITGAGAACTGTGCAAAAATAATCTTTTTCACAAAATCCAGATTCT	692
1	SEQ_31	AAATGTGTGGGCGCTGCAAGTCTCAGAAATAGCGGTGAGAAAAACAGGAGCA-CTTAAGANTGCAATCATATTTACGATATCTGTAG	784
2	SEQ_32	AAATGTGTGGGCGCACTCCAGGTTCTGAGATAGAGGCAAGAAATAGGCAATGAGAACTATTTACGATATCTGTAG	808
3	SEQ_33	AAATGTGTGGGCGCACTCCAGGTTCTGAGATAGAGGCAAGAAATAGGCAATGAGAACTATTTACGATATCTGTAG	763
4	SEQ_29	AAATGTGTGGGCGCACTCCAGGTTCTGAGATAGAGGCAAGAAATAGGCAATGAGAACTATTTACGATATCTGTAG	781
1	SEQ_31	ATCTCTTGAAATCAGCNCACATTAAGGAGCGCAGAAAGAGAAAGGCACTGNTTTAGAGAAAGCAAAATAGGANTGGAGGTCAGAG	874
2	SEQ_32	ATCTCTTGAAATCAGCNCACATTAAGGAGCGCAGAAAGAGAAAGGCACTGNTTTAGAGAAAGCAAAATAGGANTGGAGGTCAGAG	898
3	SEQ_33	ATCTCTTGAAATCAGCNCACATTAAGGAGCGCAGAAAGAGAAAGGCACTGNTTTAGAGAAAGCAAAATAGGANTGGAGGTCAGAG	853
4	SEQ_29	ATCTCTTGAAATCAGCNCACATTAAGGAGCGCAGAAAGAGAAAGGCACTGNTTTAGAGAAAGCAAAATAGGANTGGAGGTCAGAG	871
1	SEQ_31	TAGACAGTCGACGCTGGAATACCAAAAGACAGGAAACCCAACTAAATATCAAGTGA- GATGAGTATATACCACAGGACAGGAGGCCCAATA	963
2	SEQ_32	TAGACAGTCGACGCTGGAATACCAAAAGACAGGAAACCCAACTAAATATCAAGTGA- GATGAGTATATACCACAGGACAGGAGGCCCAATA	987
3	SEQ_33	TAGACAGTCGACGCTGGAATACCAAAAGACAGGAAACCCAACTAAATATCAAGTGA- GATGAGTATATACCACAGGACAGGAGGCCCAATA	942
4	SEQ_29	TAGACAGTCGACGCTGGAATACCAAAAGACAGGAAACCCAACTAAATATCAAGTGA- GATGAGTATATACCACAGGACAGGAGGCCCAATA	961
1	SEQ_31	AGAAAGAGTGTGTGATGATACCAAGGACAGGAGTCCCAAGTAAAGAGAGTGTGAGTCAAGTGTGTCCTCCCAAGAGCAAGAGCCCAAGTA	1053
2	SEQ_32	AGAAAGAGTGTGTGATGATACCAAGGACAGGAGTCCCAAGTAAAGAGAGTGTGAGTCAAGTGTGTCCTCCCAAGAGCAAGAGCCCAAGTA	1077
3	SEQ_33	AGAAAGAGTGTGTGATGATACCAAGGACAGGAGTCCCAAGTAAAGAGAGTGTGAGTCAAGTGTGTCCTCCCAAGAGCAAGAGCCCAAGTA	1032
4	SEQ_29	AGAAAGAGTGTGTGATGATACCAAGGACAGGAGTCCCAAGTAAAGAGAGTGTGAGTCAAGTGTGTCCTCCCAAGAGCAAGAGCCCAAGTA	1050
1	SEQ_31	ACGAAGAGTGTGTGATGATACCAAGGACAGGAGTCCCAAGTAAAGAGAGTGTGAGTCAAGTGTGTCCTCCCAAGAGCAAGAGCCCAAGTA	1143
2	SEQ_32	ACGAAGAGTGTGTGATGATACCAAGGACAGGAGTCCCAAGTAAAGAGAGTGTGAGTCAAGTGTGTCCTCCCAAGAGCAAGAGCCCAAGTA	1167
3	SEQ_33	ACGAAGAGTGTGTGATGATACCAAGGACAGGAGTCCCAAGTAAAGAGAGTGTGAGTCAAGTGTGTCCTCCCAAGAGCAAGAGCCCAAGTA	1122
4	SEQ_29	ACGAAGAGTGTGTGATGATACCAAGGACAGGAGTCCCAAGTAAAGAGAGTGTGAGTCAAGTGTGTCCTCCCAAGAGCAAGAGCCCAAGTA	1140
1	SEQ_31	AGAAAGAGTGTGTGATGATACCAAGGACAGGAGTCCCAAGTAAAGAGAGTGTGAGTCAAGTGTGTCCTCCCAAGAGCAAGAGCCCAAGTA	1233
2	SEQ_32	AGAAAGAGTGTGTGATGATACCAAGGACAGGAGTCCCAAGTAAAGAGAGTGTGAGTCAAGTGTGTCCTCCCAAGAGCAAGAGCCCAAGTA	1257
3	SEQ_33	AGAAAGAGTGTGTGATGATACCAAGGACAGGAGTCCCAAGTAAAGAGAGTGTGAGTCAAGTGTGTCCTCCCAAGAGCAAGAGCCCAAGTA	1210
4	SEQ_29	AGAAAGAGTGTGTGATGATACCAAGGACAGGAGTCCCAAGTAAAGAGAGTGTGAGTCAAGTGTGTCCTCCCAAGAGCAAGAGCCCAAGTA	1232

Fig. 7b

1 SEQ_36 MTVLEITLAVILTLGLAILALLTRWARKQSEMYISRYSEQSARLLDYEDGGRHAYSHUB -----ERSKUDYTPPTNSLALS 83
2 SEQ_34 MTVLEITLAVILTLGLAILALLTRWARKQSEMYISRYSEQSARLLDYEDGGRHAYSHUBSTYSDYOKRERSKRDYTFSTNSLALS 90
3 SEQ_35 MTVLEITLAVILTLGLAILALLTRWARKQSEMYISRYSEQSARLLDYEDGGRHAYSHUBSTYSDYOKRERSKRDYTFSTNSLALS 90
4 NM_006781 MTVLEITLAVILTLGLAILALLTRWARKQSEMYISRYSEQSARLLDYEDGGRHAYSHUBSTYSDYOKRERSKRDYTFSTNSLALS 90

1 SEQ_36 SSIALPQGSMSISIKLCIQTTPEPSRTAGAMQFTAPLP GATGFIHLISQTIIVQTPGPIVQVPGSN -----AGPPEAPRGPMAPILI 165
2 SEQ_34 SSIALPQGSMSISIKLCIQTTPEPSRTAGAMQFTAPLP GATGFIHLISQTIIVQTPGPIVQVPGSN -----AGPPEAPRGPMAPILI 172
3 SEQ_35 SSIALPQGSMSISIKLCIQTTPEPSRTAGAMQFTAPLP GATGFIHLISQTIIVQTPGPIVQVPGSN -----AGPPEAPRGPMAPILI 180
4 NM_006781 SSIALPQGSMSISIKLCIQTTPEPSRTAGAMQFTAPLP GATGFIHLISQTIIVQTPGPIVQVPGSN -----AGPPEAPRGPMAPILI 170

1 SEQ_36 SORTASQLAAPILISORTARIPQVHTMDSSEKITITPPVLLTGYMDEELAKKSCSKITQILKCGGTARNSQNSREHKEALKNDIIFTNSVE 256
2 SEQ_34 SORTASQLAAPILISORTARIPQVHTMDSSEKITITPPVLLTGYMDEELAKKSCSKITQILKCGGTARNSQNSREHKEALKNDIIFTNSVE 262
3 SEQ_35 SORTASQLAAPILISORTARIPQVHTMDSSEKITITPPVLLTGYMDEELAKKSCSKITQILKCGGTARNSQNSREHKEALKNDIIFTNSVE 270
4 NM_006781 SORTASQLAAPILISORTARIPQVHTMDSSEKITITPPVLLTGYMDEELAKKSCSKITQILKCGGTARNSQNSREHKEALKNDIIFTNSVE 261

1 SEQ_36 SILKSAHIKEPPEHREGKGTDLKEDKIGHEVYVDS DAGIPKQETQLKISEMSI PQGQAGQIRKSVSDVPRGQESQVKKSESGVPRGQEAQVT 343
2 SEQ_34 SILKSAHIKEPPEHREGKGTDLKEDKIGHEVYVDS DAGIPKQETQLKISEMSI PQGQAGQIRKSVSDVPRGQESQVKKSESGVPRGQEAQVT 352
3 SEQ_35 SILKSAHIKEPPEHREGKGTDLKEDKIGHEVYVDS DAGIPKQETQLKISEMSI PQGQAGQIRKSVSDVPRGQESQVKKSESGVPRGQEAQVT 360
4 NM_006781 SILKSAHIKEPPEHREGKGTDLKEDKIGHEVYVDS DAGIPKQETQLKISEMSI PQGQAGQIRKSVSDVPRGQESQVKKSESGVPRGQEAQVT 351

1 SEQ_36 KSGLVVLKQGEAQVEKSEMGVPRRQESQVKKSQSGVSKQGEAQVKKHESVVLKQGEAQVEKSELKVPKQEGQGVKTEADVPKQEVQEK 435
2 SEQ_34 KSGLVVLKQGEAQVEKSEMGVPRRQESQVKKSQSGVSKQGEAQVKKHESVVLKQGEAQVEKSELKVPKQEGQGVKTEADVPKQEVQEK 442
3 SEQ_35 KSGLVVLKQGEAQVEKSEMGVPRRQESQVKKSQSGVSKQGEAQVKKHESVVLKQGEAQVEKSELKVPKQEGQGVKTEADVPKQEVQEK 450
4 NM_006781 KSGLVVLKQGEAQVEKSEMGVPRRQESQVKKSQSGVSKQGEAQVKKHESVVLKQGEAQVEKSELKVPKQEGQGVKTEADVPKQEVQEK 441

1 SEQ_36 KSEAGVLKGPESQVKNTEVSVPETLESQVKKSESGVLKQGEAQVEKSELKVPKQEGQGVKTEADVPKQEVQEK 525
2 SEQ_34 KSEAGVLKGPESQVKNTEVSVPETLESQVKKSESGVLKQGEAQVEKSELKVPKQEGQGVKTEADVPKQEVQEK 532
3 SEQ_35 KSEAGVLKGPESQVKNTEVSVPETLESQVKKSESGVLKQGEAQVEKSELKVPKQEGQGVKTEADVPKQEVQEK 540
4 NM_006781 KSEAGVLKGPESQVKNTEVSVPETLESQVKKSESGVLKQGEAQVEKSELKVPKQEGQGVKTEADVPKQEVQEK 531

1 SEQ_36 ESEINGEKSKGRKAKANTGRKYNKKVE ----- 554
2 SEQ_34 ESEINGEKSKGRKAKANTGRKYNKKVE ----- 561
3 SEQ_35 ESEINGEKSKGRKAKANTGRKYNKKVE ----- 569
4 NM_006781 ESEINGEKSKGRKAKANTGRKYNKKVE ----- 568

Figure 8

MS4A12

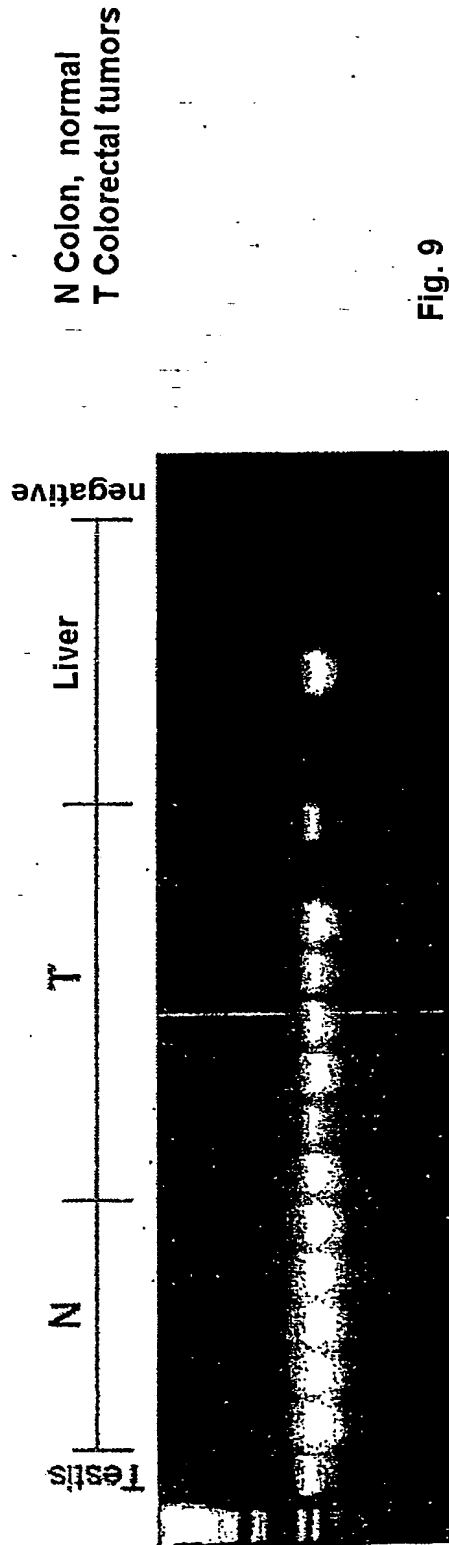


Fig. 9

BRC01

N Breast, normal
T Breast tumors

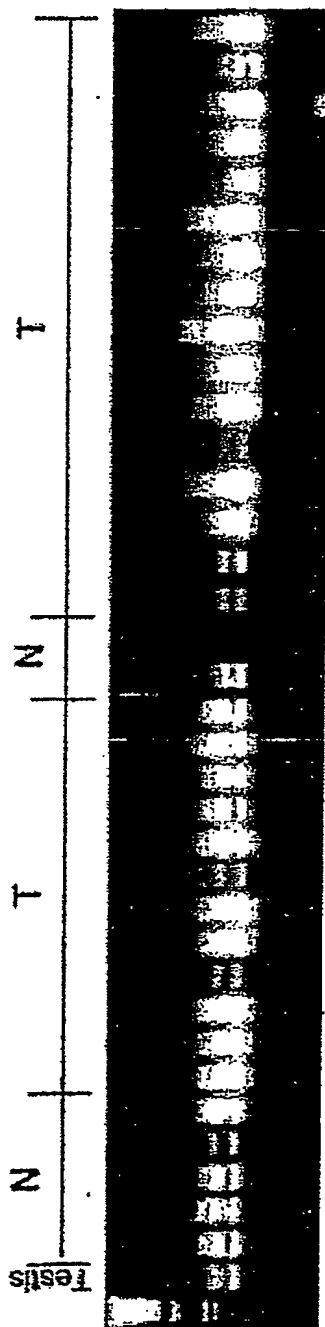
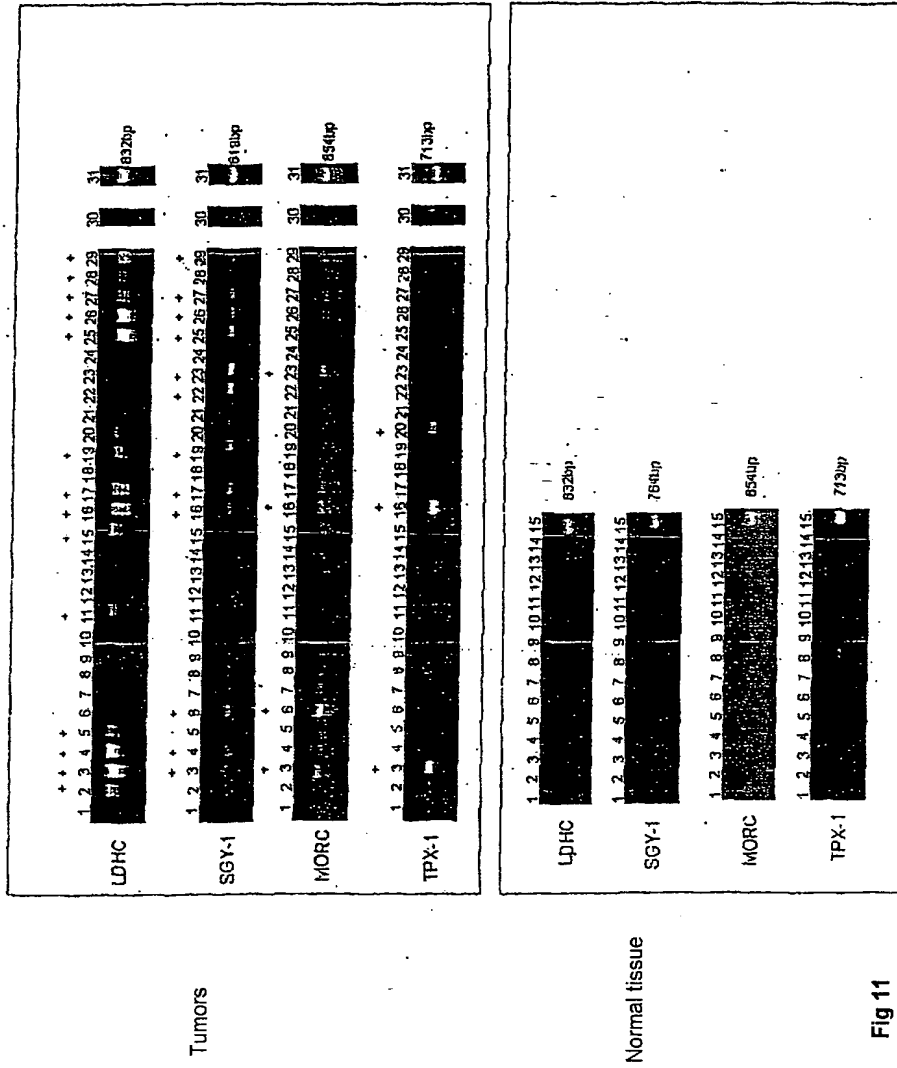
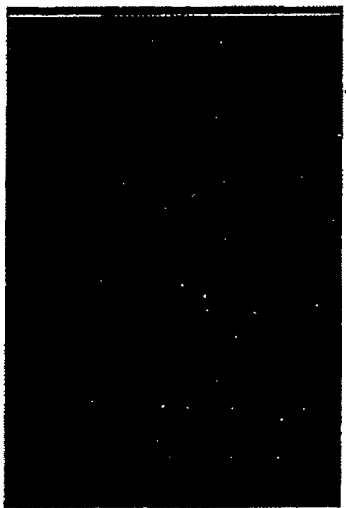


Fig. 10





anti-cytochrome c



anti-LDHC



Superposition

Fig. 12

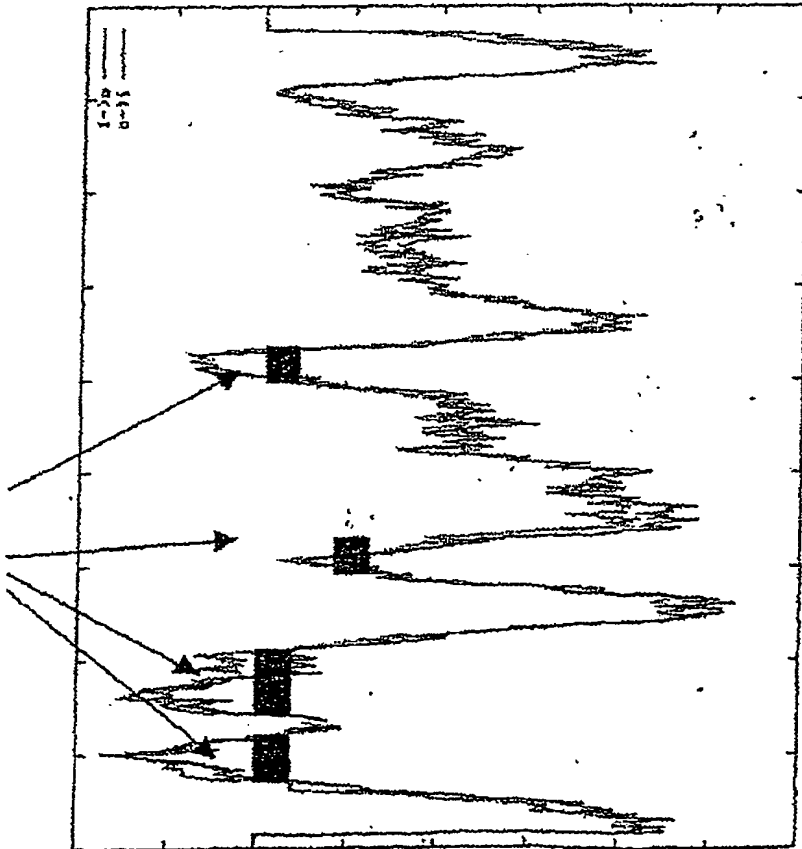
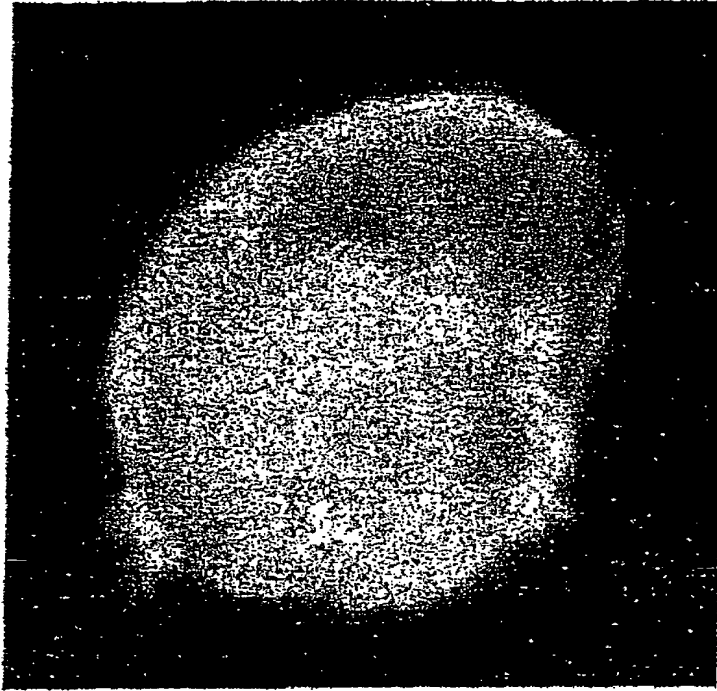


Fig. 13



Fig. 14

**This Page is Inserted by IFW Indexing and Scanning
Operations and is not part of the Official Record**

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

- ☐ BLACK BORDERS
- ☐ IMAGE CUT OFF AT TOP, BOTTOM OR SIDES
- ☒ FADED TEXT OR DRAWING
- ☐ BLURRED OR ILLEGIBLE TEXT OR DRAWING
- ☐ SKEWED/SLANTED IMAGES
- ☐ COLOR OR BLACK AND WHITE PHOTOGRAPHS
- ☐ GRAY SCALE DOCUMENTS
- ☒ LINES OR MARKS ON ORIGINAL DOCUMENT
- ☐ REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY
- ☐ OTHER: _____

IMAGES ARE BEST AVAILABLE COPY.

As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.